

Criando sua conta no Galaxy

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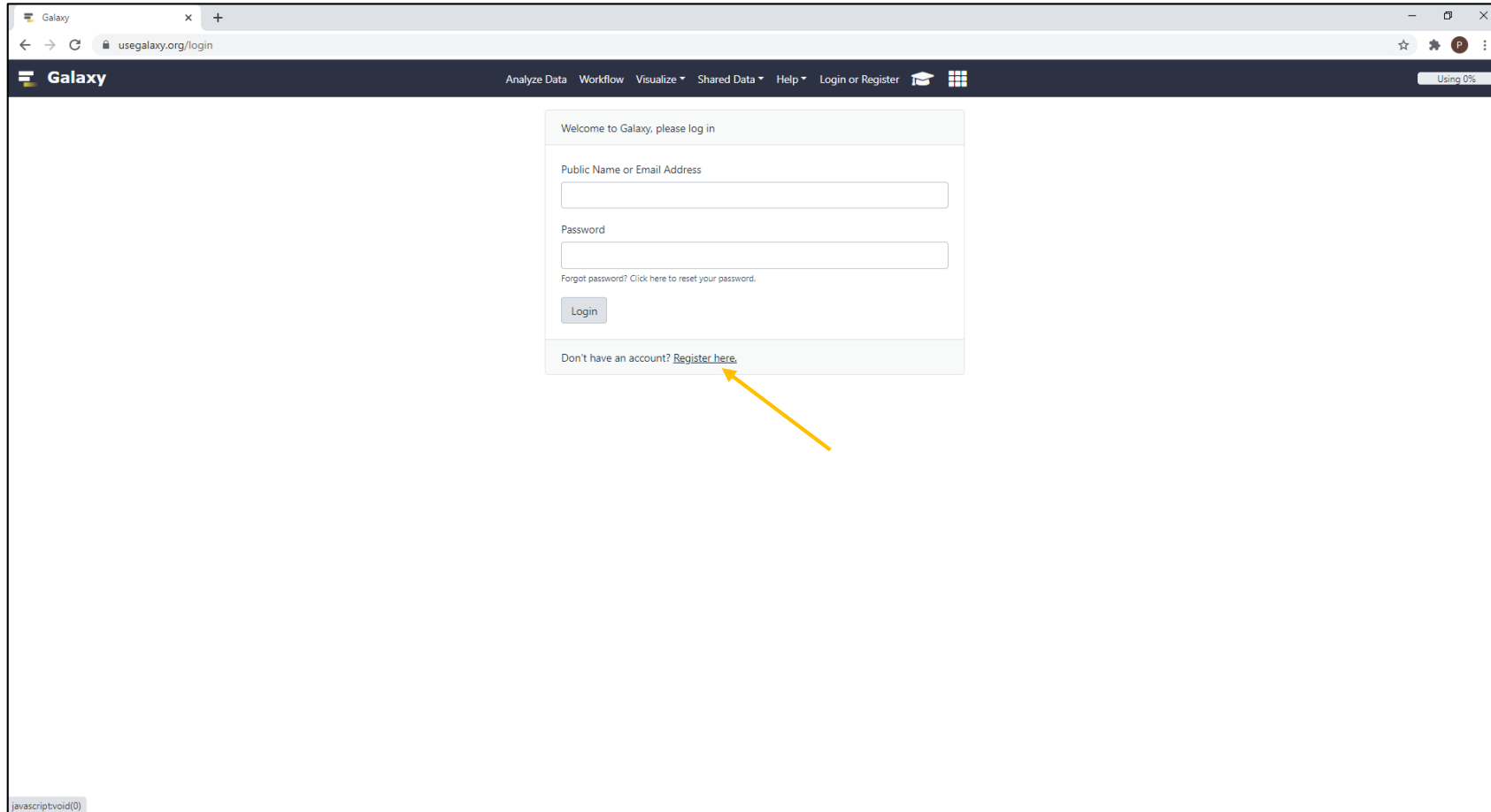
psanches@usp.br

Acesse em seu navegador

<https://usegalaxy.org>

The screenshot displays the Galaxy web interface. At the top, the browser address bar shows 'usegalaxy.org'. The main navigation bar includes 'Galaxy', 'Analyze Data', 'Workflow', 'Visualize', 'Shared Data', 'Help', and 'Login or Register'. A yellow arrow points to the 'Login or Register' link. The left sidebar contains a 'Tools' section with a search bar and 'Upload Data' button, followed by categories like 'Get Data', 'GENERAL TEXT TOOLS', 'GENOMIC FILE MANIPULATION', 'COMMON GENOMICS TOOLS', and 'GENOMICS ANALYSIS'. The central content area features a banner for the JXTX James P. Taylor Foundation, which includes a logo of sneakers and text describing the foundation's mission and a 'Donate Now' button. Below the banner is a blue information bar about SARS-CoV-2 data analysis. At the bottom, logos for PennState, Johns Hopkins University, Oregon Health & Science University, TACC, and CyVerse are displayed, along with text about the Galaxy team and infrastructure.

Crie sua conta



Insira seus dados

The image shows a screenshot of the Galaxy Web Portal login page. The browser address bar shows 'usegalaxy.org/login'. The page header includes the Galaxy logo and navigation links: 'Analyze Data', 'Workflow', 'Visualize', 'Shared Data', 'Help', 'Login or Register', and a 'Using 0%' indicator. A blue notification box at the top left states: 'Please register only one account. The usegalaxy.org service is provided free of charge and has limited computational and data storage resources. Registration and usage of multiple accounts is tracked and such accounts are subject to termination and data deletion.'

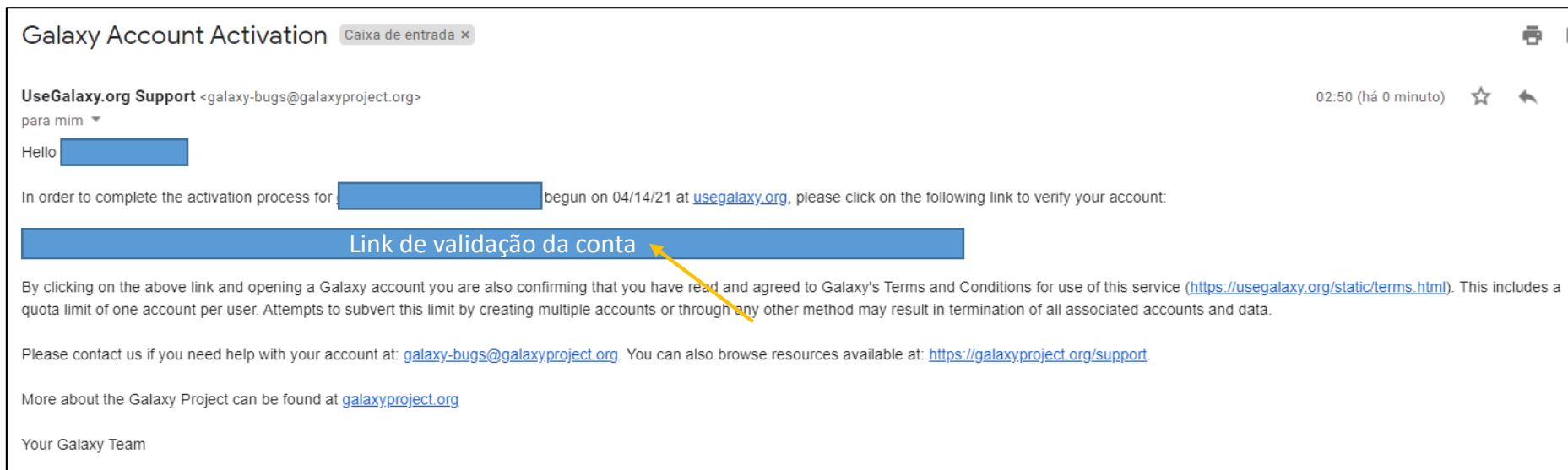
The main content area is titled 'Create a Galaxy account' and contains the following fields:

- Email Address:** A text input field with a yellow arrow pointing to it.
- Password:** A text input field with a yellow arrow pointing to it.
- Confirm password:** A text input field with a yellow arrow pointing to it.
- Public name:** A text input field with a yellow arrow pointing to it. Below this field is a note: 'Your public name is an identifier that will be used to generate addresses for information you share publicly. Public names must be at least three characters in length and contain only lower-case letters, numbers, dots, underscores, and dashes (".", "_", "-").'

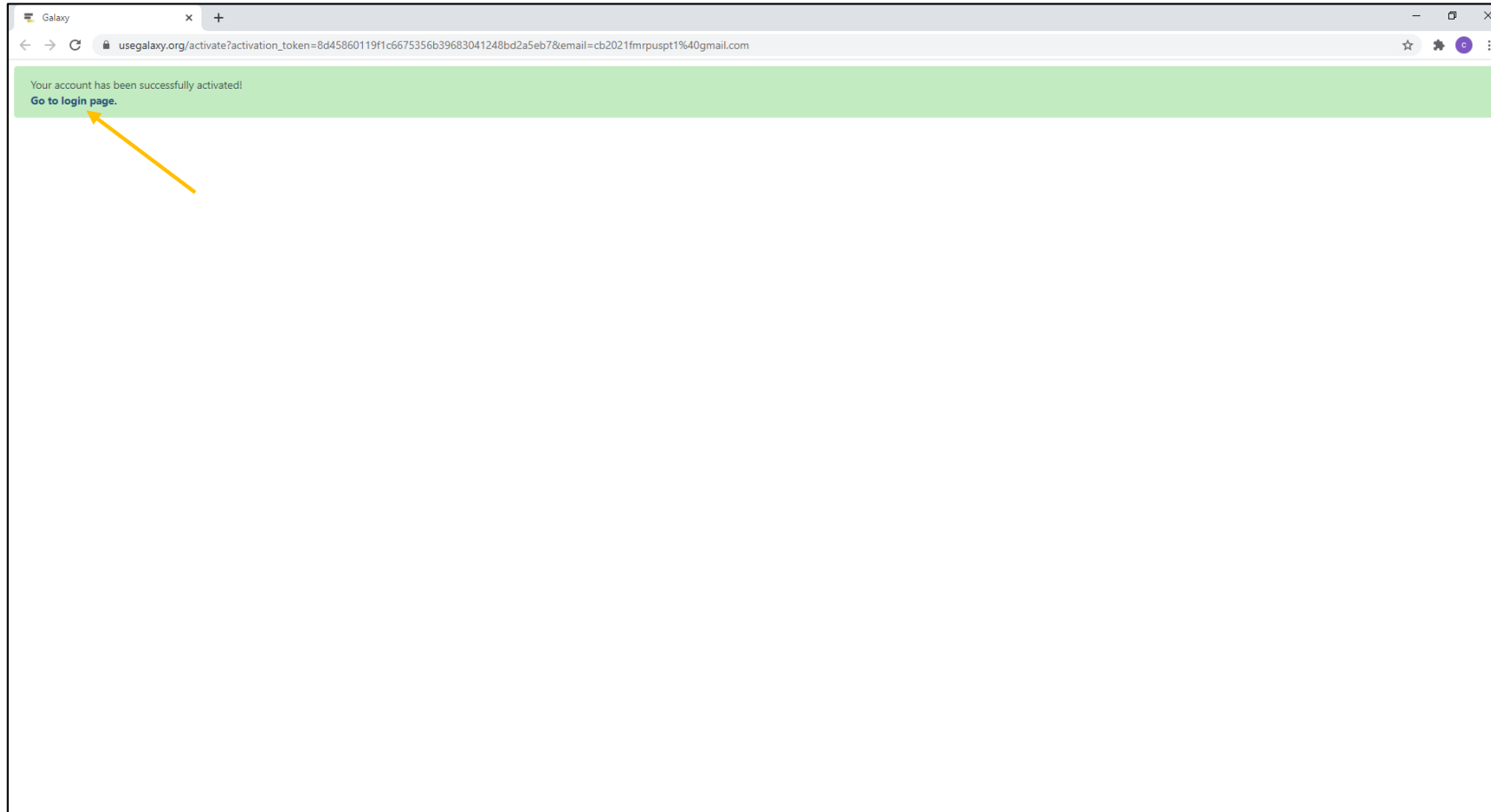
Below the fields is a 'Create' button with a yellow arrow pointing to it. At the bottom of the form, there is a link: 'Already have an account? Log in here.'

To the right of the registration form is a 'Galaxy Web Portal Service Agreement' section with three numbered paragraphs of text.

Valide sua conta Galaxy em seu e-mail



Faça o login



Pronto! Você poderá utilizar o Galaxy agora...

The screenshot displays the Galaxy web interface at usegalaxy.org/root. The main content area features a banner for the JXTX James P. Taylor Foundation. The banner includes the text "Galaxy is an open source, web-based platform for data intensive biomedical research. If you are new to Galaxy start here or consult our help resources. You can install your own Galaxy by following the tutorial and choose from thousands of tools from the Tool Shed." Below this is the JXTX logo, which consists of the letters "JXTX" in a large, bold, sans-serif font, with a pair of sneakers below it. The sneakers are white with orange and black accents, and the text "James P. Taylor Foundation" is written in a smaller font below the sneakers. The design is credited to Rebekka Palsner.

To the right of the logo, there is a text block that reads: "James Taylor (1979-2020) believed that scientific progress can best be sustained through the mentoring of students and junior faculty." Below this is a paragraph explaining the foundation's mission: "To ensure implementation of this vision, the Galaxy community has established a foundation—JXTX: The James P. Taylor Foundation for Open Science. The JXTX Foundation's mission is to (1) assist graduate students to participate in computational biology and data science conferences, and (2) organize and host mentoring sessions between senior and junior faculty members at high-profile meetings." A "Donate Now" button is located below the text.

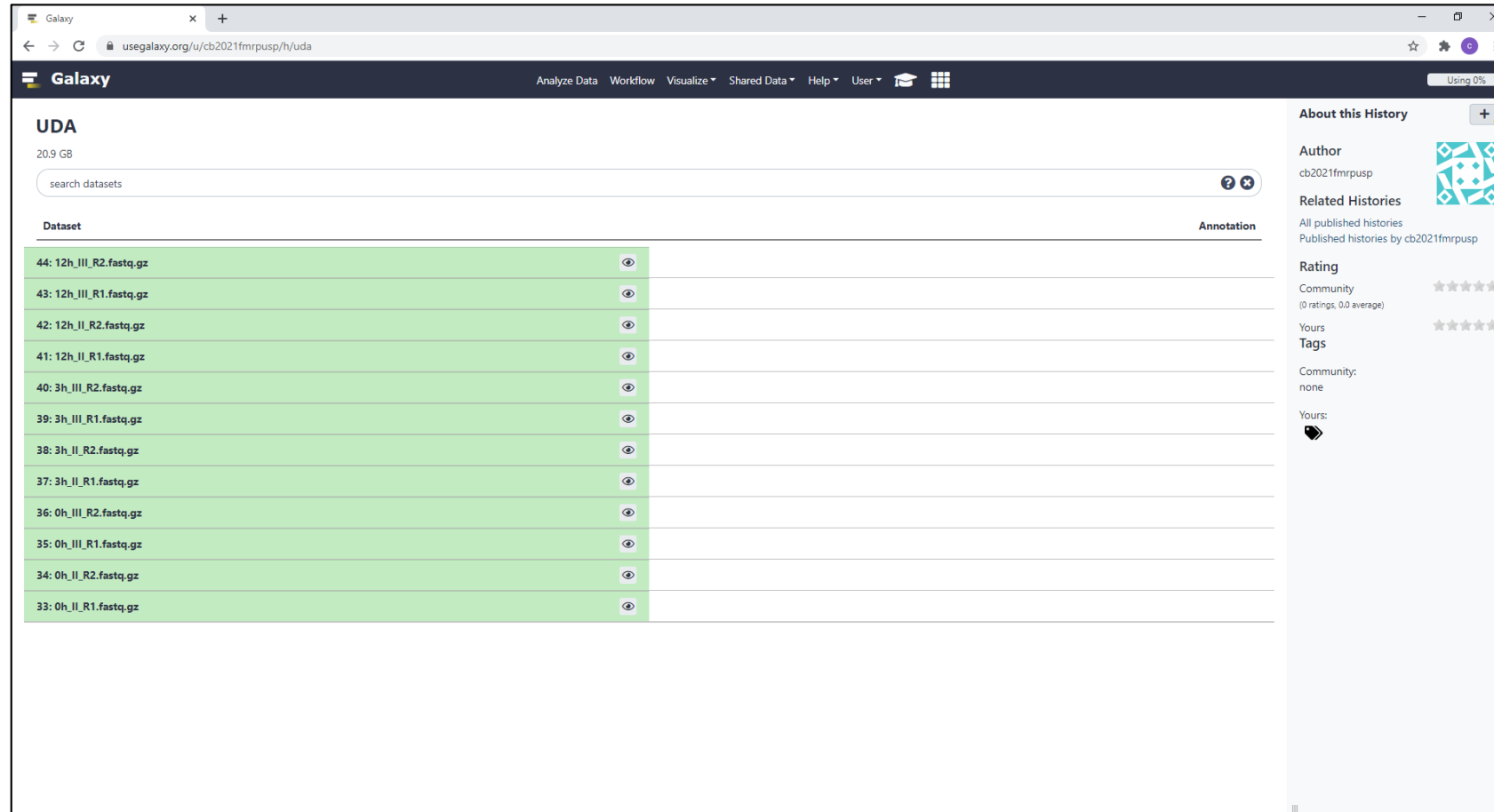
At the bottom of the banner, there is a blue bar with a white information icon and the text: "Want to learn the best practices for the analysis of SARS-CoV-2 data using Galaxy? Visit the Galaxy SARS-CoV-2 portal at covid19.galaxyproject.org"

Below the banner, there are logos for PennState, Johns Hopkins University, Oregon Health & Science University, TACC, and CyVerse. At the bottom of the page, there is a paragraph of text: "The Galaxy Team is a part of the Center for Comparative Genomics and Bioinformatics at Penn State, the Department of Biology at Johns Hopkins University and the Computational Biology Program at Oregon Health & Science University." To the right of this text is another paragraph: "This instance of Galaxy is utilizing infrastructure generously provided by CyVerse at the Texas Advanced Computing Center, with support from the National Science Foundation."

The interface also shows a left sidebar with a "Tools" section containing a search bar and an "Upload Data" button. Below this are categories like "Get Data", "Collection Operations", "GENERAL TEXT TOOLS", "Text Manipulation", "Filter and Sort", "Join, Subtract and Group", "Datamash", "GENOMIC FILE MANIPULATION", "FASTA/FASTQ", "FASTQ Quality Control", "SAM/BAM", "BED", "VCF/BCF", "Nanopore", "Convert Formats", "Lift-Over", "COMMON GENOMICS TOOLS", "Interactive tools", "Operate on Genomic Intervals", "Fetch Sequences/Alignments", "GENOMICS ANALYSIS", "Assembly", "Annotation", and "Manning". On the right side, there is a "History" section with a search bar and a message: "This history is empty. You can load your own data or get data from an external source".

Importe os dados brutos para análise

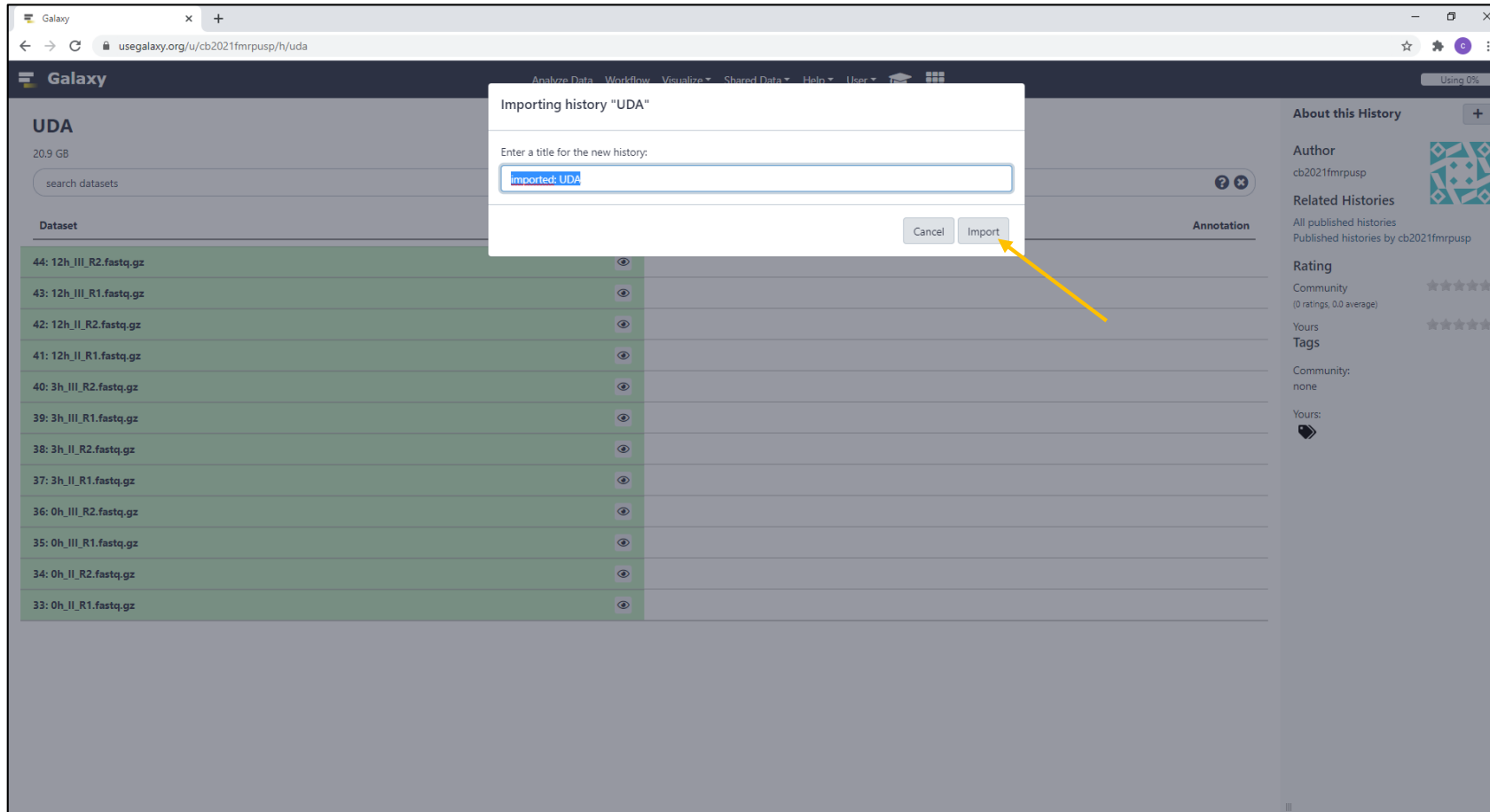
<https://usegalaxy.org/u/cb2021fmrpusp/h/uda>



The screenshot displays the Galaxy web interface. The main content area shows a history named "UDA" with a size of 20.9 GB. Below this, there is a search bar for datasets and a table of 12 datasets, each with a name and an eye icon. The datasets are listed in descending order of ID (44 to 33). The right sidebar contains information about the history, including the author (cb2021fmrpusp), related histories, and ratings. A yellow arrow points to a "+" button in the "About this History" section.

Dataset	Annotation
44: 12h_III_R2.fastq.gz	
43: 12h_III_R1.fastq.gz	
42: 12h_II_R2.fastq.gz	
41: 12h_II_R1.fastq.gz	
40: 3h_III_R2.fastq.gz	
39: 3h_III_R1.fastq.gz	
38: 3h_II_R2.fastq.gz	
37: 3h_II_R1.fastq.gz	
36: 0h_III_R2.fastq.gz	
35: 0h_III_R1.fastq.gz	
34: 0h_II_R2.fastq.gz	
33: 0h_II_R1.fastq.gz	

Confirme a importação dos dados



The screenshot shows the Galaxy web interface. A dialog box titled "Importing history 'UDA'" is centered on the screen. The dialog contains a text input field with the text "imported:UDA" and two buttons: "Cancel" and "Import". A yellow arrow points to the "Import" button. The background shows a list of datasets under the heading "UDA" (20.9 GB) and a sidebar with information about the history, including the author "cb2021fmrpusp" and a rating section.

Galaxy

usegalaxy.org/u/cb2021fmrpusp/h/uda

Galaxy

Analyze Data Workflow Visualize Shared Data Help User

Using 0%

UDA

20.9 GB

search datasets

Dataset

44: 12h_III_R2.fastq.gz	⏏
43: 12h_III_R1.fastq.gz	⏏
42: 12h_II_R2.fastq.gz	⏏
41: 12h_II_R1.fastq.gz	⏏
40: 3h_III_R2.fastq.gz	⏏
39: 3h_III_R1.fastq.gz	⏏
38: 3h_II_R2.fastq.gz	⏏
37: 3h_II_R1.fastq.gz	⏏
36: 0h_III_R2.fastq.gz	⏏
35: 0h_III_R1.fastq.gz	⏏
34: 0h_II_R2.fastq.gz	⏏
33: 0h_II_R1.fastq.gz	⏏

Annotation

About this History

Author
cb2021fmrpusp

Related Histories
All published histories
Published histories by cb2021fmrpusp

Rating
Community
(0 ratings, 0.0 average)

Yours
★★★★★

Tags
Community:
none

Yours:
🔍

Pronto! Você poderá trabalhar com os dados...

The screenshot shows the Galaxy web interface at usegalaxy.org. The main content area features a banner for the JXTX James P. Taylor Foundation, which is an open source, web-based platform for data intensive biomedical research. The banner includes the text: "Galaxy is an open source, web-based platform for data intensive biomedical research. If you are new to Galaxy start here or consult our help resources. You can install your own Galaxy by following the tutorial and choose from thousands of tools from the Tool Shed." Below this is the JXTX logo and the text "James P. Taylor Foundation" with a "Donate Now" button. A blue banner below the main content reads: "Want to learn the best practices for the analysis of SARS-CoV-2 data using Galaxy? Visit the Galaxy SARS-CoV-2 portal at covid19.galaxyproject.org".

The left sidebar contains a "Tools" section with a search bar and an "Upload Data" button. Below this are categories for "Get Data", "Collection Operations", "GENERAL TEXT TOOLS", "Text Manipulation", "Filter and Sort", "Join, Subtract and Group", "Datamash", "GENOMIC FILE MANIPULATION", "FASTA/FASTQ", "FASTQ Quality Control", "SAM/BAM", "BED", "VCF/BCF", "Nanopore", "Convert Formats", "Lift-Over", "COMMON GENOMICS TOOLS", "Interactive tools", "Operate on Genomic Intervals", "Fetch Sequences/Alignments", "GENOMICS ANALYSIS", "Assembly", "Annotation", and "Manning".

The right sidebar shows a "History" section with a search bar and a list of imported datasets. The list is highlighted with a yellow box and contains the following entries:

Dataset Name	View	Edit	Delete
44: 12h_III_R2.fastq.gz	👁	✎	✕
43: 12h_III_R1.fastq.gz	👁	✎	✕
42: 12h_II_R2.fastq.gz	👁	✎	✕
41: 12h_II_R1.fastq.gz	👁	✎	✕
40: 3h_III_R2.fastq.gz	👁	✎	✕
39: 3h_III_R1.fastq.gz	👁	✎	✕
38: 3h_II_R2.fastq.gz	👁	✎	✕
37: 3h_II_R1.fastq.gz	👁	✎	✕
36: 0h_III_R2.fastq.gz	👁	✎	✕
35: 0h_III_R1.fastq.gz	👁	✎	✕
34: 0h_II_R2.fastq.gz	👁	✎	✕
33: 0h_II_R1.fastq.gz	👁	✎	✕